

NEW SHEET

(3) Sequence Description: Figure 11A

1 ATGTCCCCTATACTAGTTATTGGAAAATTAAGGCCTTGCAACCC
5 MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro 16

49 ACTCGACTTCTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTG
ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu 32

10 97 TATGAGCGCGATGAAGGTGATAAAATGGCGAACAAAAAGTTGAATTG
TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu 48

15 145 GGTTTGGAGTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAA
GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys 64

193 TTAACACAGTCTATGCCCATCACGTTATATAGCTGACAAGCACAAC
LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn 80

20 241 ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTCAATGCTTGAA
MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu 96

289 GGAGCGGGTTTGGATATTAGATACGGTGTTCGAGAATTGCATATAGT
GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer 112

25 337 AAAGACTTTGAAACTCTCAAAGATGATTCTTAGCAAGCTACCTGAA
LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu 128

30 385 ATGCTGAAAATGTCGAAGATCGTTATGTCATAAAACATATTTAAAT
MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn 144

433 GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGAT
GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp 160

35 481 GTTGTGTTATACATGGACCCAATGTGCCTGGATGCGTTCCAAAATTA
ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu 176

NEW SHEET

(3) Sequence Description (continued): Figure 11B

529 GTTTGTTTAAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC
 ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr 192

5 577 TTGAAATCCAGCAAGTATATAGCATGGCCTTGCAAGGGCTGGCAAGGCC
 LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla 208

10 625 ACGTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGTTCCGCGT
 ThrPheGlyGlyAspHisProProLysSerAspLeuValProArg 224

15 673 GGATCCATGAGCACGATTCCCAACCTCAAAGAAAAACCAAACGTAAC
 GlySerMetSerThrIleProLysProGlnArgLysThrLysArgAsn 240

721 ACCAACCGTCGCCACAGGAATTCATCGTGACTGACTGA
 ThrAsnArgArgProGlnGluPheIleValThrAspEnd 252

NEW SHEET

(4) Sequence Description: Figure 12 A

1	ATGTCCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCC MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro	16
5	ACTCGACTTCTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTTG ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu	32
97	TATGAGCGCGATGAAGGTGATAAAATGGCGAACAAAAAGTTGAATTG TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu	48
10	GGTTTGGAGTTCCCAATCTCCTTATTATATTGATGGTGATGTTAAA GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys	64
15	TTAACACAGTCTATGCCATCAGTTATATAGCTGACAAGCACAAAC LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn	80
193	ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTCAATGCTTGAA MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu	96
20	GGAGCGGTTTGGATATTAGATACGGTGTTCGAGAATTGCATATAGT GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer	112

NEW SHEET

(4) Sequence Description (continued): Figure 12B

337 AAAGACTTGTAACTCTCAAAGTTGATTTCTTAGCAAGCTACCTGAA
LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu 128

5 385 ATGCTGAAAATGTTCGAAGATCGTTATGTCATAAACATATTAAAT
MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn 144

433 GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTGAT
GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp 160

10 481 GTTGTAAACATGGACCAATGTGCCTGGATGCGTCCCCAAATTAA
ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu 176

15 529 GTTTGTTTAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC
ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr 192

577 TTGAAATCCAGCAAGTATATAGCATGGCCTTGCAAGGCTGGCAAGCC
LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla 208

20 625 ACGTTGGTGGCGACCATCCTCCAAATCGGATCTGGTTCCCGCT
ThrPheGlyGlyAspHisProProLysSerAspLeuValProArg 224

673 GGATCCGACGTCAAGTTCCCGGGTGGCGGTCAAGATCGTTGGTGGAGTT
GlySerAspValLysPheProGlyGlyGlyGlnIleValGlyGlyVal 240

25 721 TACTTGTTGCCGCGCAGGGAATTCATCGTGACTGACTGA
TyrLeuLeuProArgArgGluPheIleValThrAspEnd 252

NEW SHEET

5

(6) Sequence Description: Figure 13A

1 ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCC
MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro 16

10 49 ACTCGACTTCTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTTG
ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu 32

97 TATGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTGAATTG
TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu 48

15 145 GGTGGAGTTCCCAATCTCCTTATTATATTGATGGTGATGTTAAA
GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys 64

20 193 TTAACACAGTCTATGCCCATCACGTTATAGCTGACAAGCACAAAC
LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn 80

241 ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTCATGCTTGAA
MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu 96

25 289 GGAGCGGTTTGGATATTAGATAACGGTGTTCGAGAATTGCATATAGT
GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer 112

30 337 AAAGACTTGAACACTCTCAAAGTTGATTTCTTAGCAAGCTACCTGAA
LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu 128

385 ATGCTGAAAATGTCGAAGATCGTTATGTCATAAACATATTAAAT
MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn 144

35 433 GGTGATCATGTAACCCATCCTGACTTCATGTTGATGACGCTCTTGAT
GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp 160

NEW SHEET

(6) Sequence Description (continued): Figure 13B

481	GTTGTTTATACATGGACCCAATGTGCCTGGATGCGTTCCAAAATTA ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu	176
5	529 GTTTGTTTAAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr	192
10	577 TTGAAATCCAGCAAGTATATAGCATGCCCTTGCAGGGCTGGCAAGCC LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla	208
15	625 ACGTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGTTCCCGCT ThrPheGlyGlyAspHisProProLysSerAspLeuValProArg	224
20	673 GGATCCAGCACGATTCCAAACCTCAAAGAAAAACCAAACGTAACACC GlySerSerThrIleProLysProGlnArgLysThrLysArgAsnThr	240
	721 AACCGTCGCCACAGGACGTCAAGTTCCCGGTGGCGGTCAAGATCGTT AsnArgArgProGlnAspValLysPheProGlyGlyGlnIleVal	256
	769 GGTGGAGTTACTTGTGCCGCGCAGGAAATTCACTCGTGAUTGACTGA GlyGlyValTyrLeuLeuProArgArgGluPheIleValThrAspEnd	271

NEW SHEET

(7) Sequence Description: Figure 14

5'-GATCCATGAGCACGATTCCCCAACCTCAAAGAAAAACCAAACGTAACACCAACC GT CGC
CCACAGG-3'

5 (8) Sequence Description: Figure 15

5'-AATT CCT GT GGG CG AC GG TT GG TG TT AC GTT GG TT TT CT TT GAG GTT GG AAT CG T
GCT CAT G-3'

(9) Sequence Description: Figure 16

5'-GATCCGACGTCAAGTTCCC GG GT GG CG GT CAG AT CG TT GG TG AG TT ACT TG TT GCG
CG CAG GG-3'

10 (10) Sequence Description: Figure 17

5'-AATT CCT GT GCG GG CA ACA AGT AAA ACT CC ACC AAC GAT CT GAC CG CC ACC CG GG AACT T
GAC GT CG-3'

15 (13) Sequence Description: Figure 18

5'-GA ATT CCT TAC CT GCG CGG CA ACA AGT AAA ACT C-3'

20 (14) Sequence Description: Figure 19

5'-GCT GG AT CC AGC AC GATT CCC AAC CT CAA AG-3'